

PATENT

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In the Application of:  
O. FAMODU ET AL.

CASE NO.: BB-1270

APPLICATION NO.: 09/831,683

CONFIRMATION NO.: 7062

GROUP ART UNIT: UNKNOWN

EXAMINER: UNKNOWN

I. A. FILING DATE: 11/09/1999

FOR: PLANT AMINOACYL-TRNA SYNTHETASES

**STATEMENT UNDER 37 CFR 1.825(d), 1.821(f), and 1.821(g)**

Commissioner for Patents  
Box PCT  
Washington, D.C. 20231

Sir:

The submission of the substitute Sequence Listing filed concurrently herewith does not include new matter.

The copy of substitute Sequence Listing in computer readable form filed concurrently herewith is identical to that currently on file, is the same as the paper copy of the substitute Sequence Listing filed concurrently herewith, and does not include new matter.

Respectfully submitted,



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Facsimile: 302-892-1026

Dated: 14 February 2003

# SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Plant Aminoacyl-tRNA Synthetases

<130> BB1270

<140> US/09/831,683

<141> 2001-05-10

<150> 60/107,789

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<212> DNA

<213> Oryza sativa

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Gln His Phe Asp Met Leu Phe Lys Ala Tyr Arg Arg Ala Gly Trp Leu	50	55	60
Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly	65	70	75
Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Ser Ser Glu	85	90	95
Val Val Arg Leu Val Asp Leu Leu Asp Glu Ala Lys Arg Arg Cys Lys	100	105	110
Ile Ala Ile Leu Glu Arg Asp Thr Thr Lys Asp Trp Ser Glu Glu Glu	115	120	125
Ile Glu Lys Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala	130	135	140
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Met Leu Asn Asp Lys Gly Asn Thr Ala Val Tyr Leu Leu Tyr Ala His	165	170	175
Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Gly Lys Asp Ile Glu Glu	180	185	190
Val Lys Arg Asn Gly Lys Ile Val Leu Asp His Glu Asp Glu Arg Ala	195	200	205
Leu Gly Leu His Leu Leu Gln Phe Pro Glu Val Phe Glu Glu Ala Cys	210	215	220
Thr Asn Leu Leu Pro Asn Phe Leu Cys Glu Tyr Leu Tyr Asn Leu Ala	225	230	235
Glu Ile Phe Thr Lys Lys Phe Tyr Ala Asn Cys Gln Val Val Gly Ser	245	250	255
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Gln Met Leu Ser Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala
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Cys Thr Asn Leu Leu Pro Ser Val Leu Cys Glu Tyr Leu Tyr Asn Leu
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 <212> PRT  
 <213> Zea mays

<400> 10

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			20					25					30			
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Leu	His	Gly	Val	Asn	Pro	Ile	Ile	Leu	Tyr	Ile	Ala	Arg	Gly	Ala	Ser	
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Ile	Ala	Ser	Leu	Ser	Gly	Lys	Asn	Asp	Ile	Glu	Phe	Gly	His	Val	Val	
65					70					75					80	
Glu	Trp	Leu	Glu	Tyr	Ala	Pro	Thr	Phe	Leu	Ser	Gly	Ser	Glu	Phe	Glu	
				85					90					95		
Asn	Ala	Cys	Leu	Phe	Val	Asp	Gly	Phe	Leu	Ala	Ser	Arg	Thr	Phe	Leu	
			100					105					110			
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Gln	Asn	Leu	Val	Arg	Trp	Phe	Asn	Ser	Ile	Asp	Ser	Glu	Tyr	Lys	Glu	
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Ala	Leu	Asn	Glu	Val	Val	Ala	Ala	Phe	Val	Gly	Lys	Arg	Gly	Ile	Gly	
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Lys	Ser	Pro	Ala	Pro	Ser	Leu	Lys	Glu	Lys	Val	His	Asp	Ser	Lys	Asp	
			180					185					190			
Pro	Ser	Ala	Pro	Glu	Val	Asp	Leu	Pro	Gly	Ala	Lys	Val	Gly	Lys	Val	
		195					200					205				
Cys	Val	Arg	Phe	Ala	Pro	Glu	Pro	Ser	Gly	Tyr	Leu	His	Ile	Gly	His	
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Ala	Lys	Ala	Ala	Leu	Leu	Asn	Lys	Tyr	Phe	Ala	Glu	Arg	Tyr	Gln	Gly	
225					230					235					240	
Arg	Leu	Ile	Val	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Ser	Lys	Glu	Ser	Asn	
				245					250					255		
Glu	Phe	Val	Glu	Asn	Leu	Leu	Lys	Asp	Ile	Glu	Thr	Leu	Gly	Ile	Lys	
		260						265					270			
Tyr	Asp	Ala	Val	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Pro	Lys	Leu	Met	Glu	
		275					280					285				
Met	Ala	Glu	Ser	Leu	Ile	Lys	Gln	Gly	Lys	Ala	Tyr	Ile	Asp	Asp	Thr	
	290					295					300					
Pro	Lys	Glu	Gln	Met	Arg	Lys	Glu	Arg	Met	Asp	Gly	Ile	Glu	Ser	Arg	
305					310					315					320	

Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met  
 325 330 335  
 Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu  
 340 345 350  
 Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg  
 355 360 365  
 Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr  
 370 375 380  
 Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val  
 385 390 395 400  
 Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr  
 405 410 415  
 Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu  
 420 425 430  
 Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu  
 435 440 445  
 Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg  
 450 455 460  
 Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala  
 465 470 475 480  
 Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu  
 485 490 495  
 Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro  
 500 505 510  
 Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe  
 515 520 525  
 Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg  
 530 535 540  
 His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn  
 545 550 555 560  
 Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ala Ile Asn Lys Gly Glu  
 565 570 575  
 Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys  
 580 585 590  
 Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu  
 595 600 605  
 Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile  
 610 615 620  
 Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser  
 625 630 635 640

Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro  
 645 650 655  
 Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn  
 660 665 670  
 Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg  
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 Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala  
 690 695 700  
 Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser  
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 <212> DNA  
 <213> Oryza sativa

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 <222> (139)  
 <223> n = A, C, G or T

<220>  
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<220>  
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 catttctaca gttgtgagga aactatagtt tccggtttct gtagttaata aagcggaatt 1860  
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<210> 12  
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 <212> PRT  
 <213> Oryza sativa

<220>  
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 <223> Xaa = ANY AMINO ACID

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 His Leu Arg Arg Pro Ser Pro Ser Ala Pro Pro Pro Pro Pro Arg Arg  
                     20                    25                    30  
 His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala  
                     35                    40                    45  
 Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr  
     50                    55                    60  
 Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp  
     65                    70                    75                    80  
 Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser  
                     85                    90                    95  
 Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly  
                     100                    105                    110  
 Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys  
                     115                    120                    125  
 Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe  
     130                    135                    140  
 Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys  
     145                    150                    155                    160  
 Asn Leu Pro Pro Val Tyr Ile Gly Lys Trp Gly Thr Ala Ser Asp Ala  
                     165                    170                    175  
 Glu Ile Gln Gln Glu Leu Glu Lys Gly Thr Pro Tyr Thr Tyr Arg Phe  
                     180                    185                    190  
 Arg Val Pro Lys Glu Gly Ser Leu Lys Ile Asn Asp Leu Ile Arg Gly  
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 Glu Val Ser Trp Asn Leu Asp Thr Leu Gly Asp Phe Val Ile Met Arg  
     210                    215                    220

Ser Asn Gly Gln Pro Val Tyr Asn Phe Cys Val Thr Val Asp Asp Ala  
 225 230 235 240  
 Thr Met Arg Ile Ser His Val Ile Arg Ala Glu Glu His Leu Pro Asn  
 245 250 255  
 Thr Leu Arg Gln Ala Leu Ile Tyr Lys Ala Leu Gly Phe Pro Met Pro  
 260 265 270  
 Ser Phe Ala His Val Ser Leu Ile Leu Ala Pro Asp Arg Ser Lys Leu  
 275 280 285  
 Ser Lys Arg His Gly Ala Thr Ser Val Gly Gln Tyr Lys Glu Met Gly  
 290 295 300  
 Tyr Leu Pro Gln Ala Met Val Asn Tyr Leu Ala Leu Leu Gly Trp Gly  
 305 310 315 320  
 Asp Gly Thr Glu Asn Glu Phe Phe Thr Ile Asp Asp Leu Val Glu Lys  
 325 330 335  
 Phe Thr Ile Asn Arg Val Asn Lys Ser Gly Ala Val Phe Asp Ala Val  
 340 345 350  
 Lys Leu Lys Trp Met Asn Gly Gln His Leu Arg Ser Phe Pro Pro Asp  
 355 360 365  
 Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr Gly Ile Leu  
 370 375 380  
 Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu Leu Leu Lys  
 385 390 395 400  
 Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu Ser Asn Leu  
 405 410 415  
 Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu Ala Lys Ser  
 420 425 430  
 Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu Ile Ser Ala  
 435 440 445  
 Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly Arg Asp Gly  
 450 455 460  
 Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys Arg Lys Gly  
 465 470 475 480  
 Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly Lys Leu His  
 485 490 495  
 Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr  
 500 505 510  
 Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg  
 515 520 525  
 Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln  
 530 535 540  
 Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser

545

550

555

&lt;210&gt; 13

&lt;211&gt; 731

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;400&gt; 13

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&lt;210&gt; 14

&lt;211&gt; 404

&lt;212&gt; PRT

&lt;213&gt; Glycine max

&lt;400&gt; 14

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Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly
          20              25              30

Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr
          35              40              45

Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
  50              55              60

Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg
  65              70              75              80

Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His
          85              90              95

Gln Ser Gly His Val Tyr Arg Cys Phe Cys Ser Asn Glu Glu Leu Glu
          100              105              110

Lys Met Lys Glu Asp Ala Lys Leu Lys Gln Leu Pro Pro Val Tyr Thr
          115              120              125

Gly Lys Trp Ala Ser Ala Thr Asn Glu Glu Val Glu Glu Glu Leu Ala
          130              135              140

Lys Gly Thr Pro Tyr Thr Tyr Arg Phe Arg Val Pro Lys Gly Ser Leu
          145              150              155              160

Lys Ile Asn Asp Gln Ile Arg Gly Glu Val Ser Trp Asn Leu Asp Thr
          165              170              175

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Leu Gly Asp Phe Val Ile Met Arg Ser Asn Gly Gln Pro Val Tyr Asn  
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 Phe Cys Val Thr Val Asp Asp Ala Thr Met Ala Ile Ser His Val Ile  
 195 200 205  
 Arg Ala Glu Glu His Leu Pro Asn Thr Leu Arg Gln Ala Leu Ile Tyr  
 210 215 220  
 Lys Ala Leu Gly Phe Pro Met Pro His Phe Ala His Val Ser Leu Ile  
 225 230 235 240  
 Leu Ala Pro Asp Arg Ser Lys Leu Ser Lys Arg His Gly Ala Thr Ser  
 245 250 255  
 Val Gly Gln Phe Arg Asp Met Gly Tyr Leu Pro Gln Ala Met Val Asn  
 260 265 270  
 Tyr Leu Ala Leu Leu Gly Trp Gly Asp Gly Thr Glu Asn Glu Phe Phe  
 275 280 285  
 Thr Leu Glu Gln Leu Val Glu Lys Phe Thr Ile Glu Arg Val Asn Lys  
 290 295 300  
 Ser Gly Ala Ile Phe Asp Ser Thr Lys Leu Arg Trp Met Asn Gly Gln  
 305 310 315 320  
 His Leu Arg Ser Leu Pro Ser Glu Glu Leu Asn Arg Ile Ile Gly Glu  
 325 330 335  
 Arg Trp Lys Asp Ala Gly Ile Ala Thr Glu Ser Gln Gly Ile Phe Ile  
 340 345 350  
 Gln Asp Ala Val Leu Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp  
 355 360 365  
 Ser Glu Lys Ala Leu Ser Ser Leu Leu Ser Tyr Pro Leu Tyr Glu Thr  
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 385 390 395 400  
 Val Ala Lys Ser

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 <213> Triticum aestivum

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 gccctcttca attacctgat tgcaaaagct acacgcggta aattcatcct acgcatagag 240  
 gacacagatn agtcaaggac tggttcctggt gcgattgaaa aactctgcgc tgntttgaga 300  
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 aaaaatctca aaagactttt aangttataa aaaaaaacnc nccataa 407

<210> 16  
 <211> 79  
 <212> PRT  
 <213> Triticum aestivum

<220>  
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 <222> (55)  
 <223> Xaa = ANY AMINO ACID

<220>  
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 <222> (69)  
 <223> Xaa = ANY AMINO ACID

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 Leu Phe Asn Tyr Leu Ile Ala Lys Ala Thr Arg Gly Lys Phe Ile Leu

35

40

45

Arg Ile Glu Asp Thr Asp Xaa Ser Arg Thr Val Pro Gly Ala Ile Glu  
50 55 60

Lys Leu Cys Ala Xaa Leu Arg Trp Gly Gly Leu Lys Arg Asp Lys  
65 70 75

&lt;210&gt; 17

&lt;211&gt; 2387

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;400&gt; 17

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&lt;211&gt; 495

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 18





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      20             25             30

Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
      35             40             45

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
      50             55             60

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
      65             70             75             80

Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val
      85             90             95

Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser

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100					105					110					
Gly	Glu	Ala	Val	Ala	Asp	Leu	Lys	Gln	Leu	Phe	Ser	Leu	Ala	Glu	Lys
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Ile	Gly	Tyr	Ser	Lys	Trp	Leu	Gln	Phe	Asp	Ala	Ser	Val	Val	Arg	Gly
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Leu	Ala	Tyr	Tyr	Thr	Gly	Ile	Val	Phe	Glu	Gly	Phe	Asp	Arg	Glu	Gly
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Lys	Leu	Arg	Ala	Ile	Cys	Gly	Gly	Gly	Arg	Tyr	Asp	His	Leu	Phe	Ser
				165					170					175	
Thr	Phe	Gly	Ala	Asp	Asp	Ile	Ala	Ala	Cys	Gly	Phe	Gly	Phe	Gly	Asp
			180					185						190	
Ala	Ser	His	Ser	Gly	Ile	Ala	Gln	Lys	Arg	Xaa	Val	Cys	Tyr	Arg	Glu
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 tgcatactac acagggattg tttttgaggc ttttgatagg gaaggggaac tgagagcgat 420  
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 gccagcatct agtggttgcac cctgtctgcg gaagaagggc agatctgtag acctgttaga 660  
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Phe Thr Gln Val Cys Val Ile Val Asp Lys Leu Gly Lys Leu Ser Arg  
35 40 45

Glu Glu Ile Glu Lys Glu Leu Ile Ser Thr Gly Leu Ser Ser Glu Ala  
50 55 60

Val Gln Gly Ile Ile Glu Val Leu Ser Leu Lys Ser Leu Ser Lys Leu  
65 70 75 80

Glu Glu Val Leu Gly Ser Gly Val Glu Ala Val Ala Asp Leu Lys Lys  
85 90 95

Leu Phe Ser Leu Ala Glu Gln Tyr Gly Tyr Ser Asp Trp Ile Cys Phe  
100 105 110

Asp Ala Ser Val Val Arg Gly Leu Ala Tyr Tyr Thr Gly Ile Val Phe  
115 120 125

Glu Ala Phe Asp Arg Glu Gly Glu Leu Arg Ala Ile Cys Gly Gly Gly  
130 135 140

Arg Tyr Asp Arg Leu Leu Ser Thr Phe Gly Thr Glu Asp Val Pro Ala  
145 150 155 160

Cys Gly Phe Gly Phe Gly Asp Ala Val Ile Val Glu Leu Leu Lys Glu  
165 170 175

Lys Gly Leu Leu Pro Asp Leu Pro Arg Gln Ile Asp Asp Ile Val Phe  
180 185 190

Pro Leu Asp Glu Glu Leu Glu Gly Pro Ala Ser Ser Val Ala Ser Cys  
195 200 205

Leu Arg Lys Lys Gly Arg Ser Val Asp Leu Val Glu Asp Lys Arg Leu  
210 215 220

Lys Trp Val Phe Lys His Ala Glu Arg Ile Asn Ala Ser Arg Leu Ile  
225 230 235 240

Leu Val Gly Lys Ser Glu Trp Glu Arg Gly Met Val Arg Val Lys Ile  
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 ttccgaaccc gcagtactga ggttggttca ttggtagagc tacttgatga ggctaaatct 420  
 cggagcaaat cagaactact acaacggctc actgaaaatg gcaaaattgt tgactggacg 480  
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His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr  
35 40 45

Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln  
50 55 60

Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe  
65 70 75 80

Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa  
85 90 95

Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Phe Leu  
100 105 110

Val Gln Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
115 120 125

Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu  
130 135 140

Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Xaa Glu Leu Glu Gln  
145 150 155 160

Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu Lys  
165 170 175

Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Met Leu Ser  
180 185 190

Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile  
195 200 205

Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val Xaa Asp  
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 ggttttgggg attaccagtg caacaatgct atgagtgtat tttcaagaat aagaggatcc 180  
 gcaacaaact tccgtaacct catggcagtt gggcaggcaa ttgcaaataa cctccccag 240  
 tcaaataatta tcgaatccat ctctgttgcc gganctggtt acattaacat aacgttatcc 300  
 agcaattgga ttgcacagag gatacaaaga catgcttggg tgtgggaatc aaaacatggg 360  
 gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc 420  
 aaaaagaana tgcaagttgg gcaataatna aggncaacaa taaatngggg natancccaa 480  
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 Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro Met Ala Val Gly Gln Ala  
                   20                  25                  30  
 Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val  
                   35                  40                  45  
 Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala  
                   50                  55                  60  
  
 Gln Arg Ile Gln  
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tatgttacag atattgggca gcaacagcac tttgatatnc tattnaaggc ctataggcgt 180  
gcaggtttgt taccaaagga tgagaatgca tatccaaaat gtactcatat aggttttggt 240  
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gttgattact tgatgaagct aaaangcgt gtaaaattgc cntcttgaaa cgtgatacaa 360  
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20 25 30  
Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln  
35 40 45  
Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu  
50 55 60  
Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly  
65 70 75 80  
Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa  
85 90 95  
Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys  
100 105 110  
Leu Pro Ser  
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 <221> unsure  
 <222> (555)  
 <223> n = A, C, G or T

<400> 29  
 tgttttttcaa ggctgccagg atggctgggtt ggcttccaga tccaaaggaa aagaagttcc 60  
 caaaaacgag tcatgttggg tttggccttg ttcttggagc agatggcaag cgcttccgaa 120  
 ctctgtagtac tgaggttggt cggttgggaa gacctacttg atgaggctaa atctcgaagt 180  
 aaatcaagaa cttctccaag cgtctcactg gaaaatggta aaattgttga ctggactgat 240  
 gaaggaacta agagcaaact tcaaaaggca gtaagatatg gcgctgtcaa agtatgcggg 300  
 tctgaaagaa taaccgactg actaattaca cttcaacttt gattcaagan ctaagtgaca 360  
 agggaaatac tgctgtcnac ttcaataagc caagcccgta cctcccanca ttcnaaaacc 420  
 caacatgggtg tnnaaaacta aaangatggg anattccncc tgccanccaa atagctgcct 480  
 gggacgnact aacngtatgc aanatgttaa aaggatgaca acncttccaa tgtcngggng 540  
 aaactatnac taccnaagta aaagt 565

<210> 30  
 <211> 33  
 <212> PRT  
 <213> Triticum sp.

<400> 30  
 Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu  
 1 5 10 15  
 Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
 20 25 30

Leu

<210> 31  
 <211> 546  
 <212> DNA  
 <213> Oryza sp.

<220>  
 <221> unsure  
 <222> (448)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (512)  
 <223> n = A, C, G or T

<400> 31  
 atcactattt cccctgatg tactcatcaa gagttttgag gatagatgga aggacacagg 60  
 cattctccag gagtctgaaa gtgggttttg taaagaagcg gctgagcttt tgaaggatgg 120  
 catcgatttg atcaactgat ctgacgcagc cctttcaaac ctgttgctgt atcccccca 180  
 tgctacatta agcagtgat aagctaaatc tgtggtgcaa gacaagcttt ctgaggttgc 240  
 atcaggactc atttctgctt atgatagcgg tgaactttgt caagcactag ctgagggccg 300  
 tgatggttg cagaagtggg tgaaaatttt tggcaaatca cttaaaagaa agggaaagtc 360  
 actctttatg ccgctccgtg tactgctgac tggcaagctt catgggctg acatgggctg 420



caccgtagtc ctcatacaca aagccggnac tgtggagcgg tcaactcaaca atccgggtttc 480  
 gtaaattctcg acgagagggtc agaattcctga angagtggag tggagtcact ggtacaggac 540  
 aagatc 546

<210> 32  
 <211> 147  
 <212> PRT  
 <213> Oryza sp.

<400> 32  
 Pro Pro Asp Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr  
     1                    5                    10                    15  
 Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu  
                     20                    25                    30  
 Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu  
             35                    40                    45  
 Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu  
             50                    55                    60  
 Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu  
             65                    70                    75                    80  
 Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly  
                     85                    90                    95  
 Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys  
             100                    105                    110  
 Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly  
             115                    120                    125  
 Lys Leu His Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys  
             130                    135                    140  
 Ala Gly Thr  
 145

<210> 33  
 <211> 524  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (386)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (423)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (459)  
 <223> n = A, C, G or T

<220>

<221> unsure  
 <222> (481)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (483)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (486)  
 <223> n = A, C, G or T

<400> 33  
 aaatggcgct gttgtgtggc ggcattgcat ggtcgaaggt gatagttcct cccattttcc 60  
 accactctca caccctctgc accttcttct tccaacgacg ccgtttctca gtctctgtct 120  
 tctccgaaca accaccaccc gttcgcgttc gtttcgctcc ttctcccacc ggaaacctcc 180  
 acgtcggcgg tgcccgaacg gccctcttca actacttgtt cgcaagggtc aaagggtgga 240  
 aatttgtgtc gagaattgag gacactgact tggagaggtc caagtaggga gtctgaggag 300  
 gccatgctca aagatcttct ttggcttgga cttgattggg atgaagggcc tgggtgttgg 360  
 aggggattat ggtccttaaa aggcantctg agaaggaatt ccttatacaa acaatatgcc 420  
 ggngaaacta cacaaatccg ggcaagttta accgctgcnt tctggtccaa agagggaact 480  
 nanagnaat gaaaggaggt tgctaaacta aagcaactgg cccc 524

<210> 34  
 <211> 94  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> UNSURE  
 <222> (63)  
 <223> Xaa = ANY AMINO ACID

<400> 34  
 Gln Arg Arg Arg Phe Ser Val Ser Ala Leu Ser Glu Gln Pro Pro Pro  
 1 5 10 15  
 Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly  
 20 25 30  
 Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly  
 35 40 45  
 Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser  
 50 55 60  
 Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu  
 65 70 75 80  
 Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro  
 85 90

<210> 35  
 <211> 506  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure

<222> (18)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (483)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (505)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (506)  
<223> n = A, C, G or T

<400> 35  
ggaacatgga tattattngt gttcccgggg ttatggctga agcagagctt atagcttcta 60  
tcgtcacttt gtttaagcga ataggaatta cagaatcaga tgtcggattt aagggtttcca 120  
gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaaat ttatttggca 180  
aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240  
tgaaagctgt tggcttatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300  
agtcattgac cgagtttagaa gagagacttg ggagagtggg gaagcagttg ctgatctgaa 360  
acagtattct cccttgctga aaaaattggg tactctaaat ggttcaattt gatgatagtt 420  
gttcgaggtc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480  
gcntctgtgt gtgtcaatac attggnn 506

<210> 36  
<211> 48  
<212> PRT  
<213> Glycine max

<400> 36  
Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu  
1 5 10 15  
Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile  
20 25 30  
Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu  
35 40 45

<210> 37  
<211> 577  
<212> DNA  
<213> Triticum sp.

<220>  
<221> unsure  
<222> (140)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (370)  
<223> n = A, C, G or T

<220>  
<221> unsure

<222> (411)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (413)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (469)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (481)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (504)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (575)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (530)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (551)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (556)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (564)  
<223> n = A, C, G or T

<400> 37  
cttgggatta catcttctga tgtgggggatc agactgtcca gccgaaaggt tctacaggcc 60  
gtggttgata tgtactccgt accacaacac ttgtttactc aagtttgtgt tattgttgac 120  
aagctgggga aactgagtan ggaagaaatt gagaaggaaat tgatttcaac tgggctgtca 180  
tctgaagcag tacagggcat cattgaagtg ctctctctca agtcactgtc caaacttgaa 240  
gaggtgctag gctcagggtgt tgaagccgtt gctgacttga agaacctctt ctgccttgct 300  
gagcaatatg gttattctga ttggatctgt ttcgatgcat ctggtgttcg tggccttgca 360  
tactacacan gggattgttt ttgaggcttt tgataggga gggaaactga nancatttgt 420  
ggtggggggg aggtatgaca ggctacgtca acatttggaa ctgaagatnt ccacctgtg 480  
nctttggatt tggaatcctg tcanagtga ctcnnaaga aaggtctttn ctacctgcac 540  
tcaaataata nattgntcca ttgncaagac ttggggg 577

<210> 38

<211> 46  
<212> PRT  
<213> Triticum sp.

<220>  
<221> UNSURE  
<222> (38)  
<223> Xaa = ANY AMINO ACID

<400> 38  
Ile Arg Leu Ser Ser Arg Lys Val Leu Gln Ala Val Leu Asp Met Tyr  
1 5 10 15

Ser Val Pro Gln His Leu Phe Thr Gln Val Cys Val Ile Val Asp Lys  
20 25 30

Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile  
35 40 45